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RAW SEQUENCE LISTING

DATE: 03/12/2002

PATENT APPLICATION: US/09/873,829

TIME: 09:54:51

Input Set : N:\Crf3\RULE60\09873829.raw

Output Set: N:\CRF3\03122002\I873829.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Choi, Yongwon

6 Wong, Brian

7 Josien, Regis

8 Steinman, Ralph

10 (ii) TITLE OF INVENTION: A PROTEIN BELONGING TO THE INF SUPERFAMILY

11 INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING

SAME, AND

12 METHODS OF USE THEREOF

14 (iii) NUMBER OF SEQUENCES: 18

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Klauber & Jackson

18 (B) STREET: 411 Hackensack Avenue, 4th Floor

19 (C) CITY: Hackensack

20 (D) STATE: New Jersey

21 (E) COUNTRY: USA

22 (F) ZIP: 07601

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: IBM PC compatible

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/873,829

C--> 32 (B) FILING DATE: 04-Jun-2001

33 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 09/210,115

37 (B) FILING DATE:

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Jackson Esq., David A.

42 (B) REGISTRATION NUMBER: 26,742

43 (C) REFERENCE/DOCKET NUMBER: 600-1-200 CIP N

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: 201-487-5800

47 (B) TELEFAX: 201-343-1684

48 (C) TELEX: 133521

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 1823 base pairs

55 (B) TYPE: nucleic acid

56 (C) STRANDEDNESS: double

57 (D) TOPOLOGY: linear

ENTERED

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59      (ii) MOLECULE TYPE: cDNA
61      (iii) HYPOTHETICAL: NO
63      (vi) ORIGINAL SOURCE:
64          (A) ORGANISM: Homo sapiens
66      (ix) FEATURE:
67          (A) NAME/KEY: CDS
68          (B) LOCATION: 1..738
71      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
73 CAG ATG GAT CCT AAT AGA ATA TCA GAA GAT GGC ACT CAC TGC ATT TAT      48
74 Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
75      1          5          10          15
77 AGA ATT TTG AGA CTC CAT GAA AAT GCA GAT TTT CAA GAC ACA ACT CTG      96
78 Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
79      20          25          30
81 GAG AGT CAA GAT ACA AAA TTA ATA CCT GAT TCA TGT AGG AGA ATT AAA      144
82 Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
83      35          40          45
85 CAG GCC TTT CAA GGA GCT GTG CAA AAG GAA TTA CAA CAT ATC GTT GGA      192
86 Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
87      50          55          60
89 TCA CAG CAC ATC AGA GCA GAG AAA GCG ATG GTG GAT GGC TCA TGG TTA      240
90 Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
91      65          70          75          80
93 GAT CTG GCC AAG AGG AGC AAG CTT GAA GCT CAG CCT TTT GCT CAT CTC      288
94 Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
95      85          90          95
97 ACT ATT AAT GCC ACC GAC ATC CCA TCT GGT TCC CAT AAA GTG AGT CTG      336
98 Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
99      100         105         110
101 TCC TCT TGG TAC CAT GAT CGG GGG TGG GGT AAG ATC TCC AAC ATG ACT      384
102 Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
103      115         120         125
105 TTT AGC AAT GGA AAA CTA ATA GTT AAT CAG GAT GGC TTT TAT TAC CTG      432
106 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
107      130         135         140
109 TAT GCC AAC ATT TGC TTT CGA CAT CAT GAA ACT TCA GGA GAC CTA GCT      480
110 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
111      145         150         155         160
113 ACA GAG TAT CTT CAA CTA ATG GTG TAC GTC ACT AAA ACC AGC ATC AAA      528
114 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
115      165         170         175
117 ATC CCA AGT TCT CAT ACC CTG ATG AAA GGA GGA AGC ACC AAG TAT TGG      576
118 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
119      180         185         190
121 TCA GGG AAT TCT GAA TTC CAT TTT TAT TCC ATA AAC GTT GGT GGA TTT      624
122 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
123      195         200         205
125 TTT AAG TTA CGG TCT GGA GAG GAA ATC AGC ATC GAG GTC TCC AAC CCC      672
126 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro

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127      210      215      220
129 TCC TTA CIG GAT CCG GAT CAG GAT GCA ACA TAC TTT GGG GCT TTT AAA      720
130 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
131 225      230      235      240
133 GTT CGA GAT ATA GAT TGA GCCCCAGTTT TTGGAGTGTT ATGTAATTC      768
134 Val Arg Asp Ile Asp *
135      245
137 TGGATGTTTG GAAACATTTT TAAAAACAAG CCAAGAAAGA TGATATATAGG TGTGTGAGAC      828
139 TACTAAGAGG CATGGCCCCA CCGTACACGA CTCAGTATCC ATGCCTTGA CCTGTGAGAG      888
141 AACACGCGTA TTTACAGCCA GTGGGAGATG TTAGACTCAT GGIGTGTTAC ACAATGGTTT      948
143 TTAATTTTIG TAAATGAATC CTAGAATTAA ACCAGATTGG AGCAATTACG GGTTGACCTT      1008
145 ATGAGAAACT GCAATGGGGC TATGGGAGGG GTTGGTCCCT GGTGATGTGC CCGTTGCGAG      1068
147 CTGAAGTGGG GAGGGGTGCA TCTAGCGCAA TTGAAGGATC ATCTGAAGGG GCAAAATTCCT      1128
149 TTGAATTGTT ACATCATGCT GGAACCTGCA AAAAATACTT TTCTAATGA GGAGAGAAAA      1188
151 TATATGTATT TTTATATAAT ATCTAAAGTT ATATTCAGA TGTAATGTTT TCTTTGCAAA      1248
153 GTATTGTAAA TTATATTTGT GCTATAGTAT TTGATTCAAA ATATTTAAAA ATGCTTGCT      1308
155 GTTGACATAI TTAATGTTTT AAAATGTACAG ACATATTTAA CTGGTGCCTT TTGTAAATTC      1368
157 CCTGGGGAAA ACTTGCAGCT AAGGAGGGGA AAAAATGTTG TTTCTAATA TCAAATGCAG      1428
159 TATATTTCTT CGTCTTTTTT AAGTTAATAG ATTTTTTCAG ACTTGTCAAG CCTGTGCAAA      1488
161 AAAATTAATA TGGATGCCCT GAATAATAAG CAGGATGTTG GCCACCAGGT GCGTTTCAAA      1548
163 TTAGAAACTT AATGACTTTT AGAAAGCTGA CATTGCCAAA AAGGATACAT AATGGGCCAC      1608
165 TGAAATCTGT CAAGAGTAGT TATATAATTG TTGAACAGGT GTTTTTCCAC AAGTGCCGCA      1668
167 AATGTACCTT TTTTTGTTT TTTCAAAAT AGAAAAGTTA TTAGTGGTTT ATCAGCAAAA      1728
169 AAGTCCAATT TTAATTTAGT AAATGTATC TTATACTGTA CAATAAAAAC ATTGCCTTTG      1788
171 AATGTTAATT TTTGGTACA AAAGTCGACG GCCGC      1823
174 (2) INFORMATION FOR SEQ ID NO: 2:
176 (i) SEQUENCE CHARACTERISTICS:
177 (A) LENGTH: 245 amino acids
178 (B) TYPE: amino acid
179 (D) TOPOLOGY: linear
181 (ii) MOLECULE TYPE: protein
183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
185 Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
186 1      5      10      15
188 Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
189      20      25      30
191 Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
192      35      40      45
194 Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
195      50      55      60
197 Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
198 65      70      75      80
200 Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
201      85      90      95
203 Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
204      100      105      110
206 Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
207      115      120      125
209 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu

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210      130      135      140
212 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
213 145      150      155      160
215 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
216      165      170      175
218 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
219      180      185      190
221 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
222      195      200      205
224 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
225      210      215      220
227 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
228 225      230      235      240
230 Val Arg Asp Ile Asp
231      245
233 (2) INFORMATION FOR SEQ ID NO: 3:
235 (i) SEQUENCE CHARACTERISTICS:
236 (A) LENGTH: 2237 base pairs
237 (B) TYPE: nucleic acid
238 (C) STRANDEDNESS: double
239 (D) TOPOLOGY: linear
241 (ii) MOLECULE TYPE: cDNA
243 (iii) HYPOTHETICAL: NO
245 (vi) ORIGINAL SOURCE:
246 (A) ORGANISM: Mus musculus
248 (ix) FEATURE:
249 (A) NAME/KEY: CDS
250 (B) LOCATION: 142..1092
253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
255 CCCACGTCGCC GGGGAGCCAC TGCCAGGACC TTGTGAACC GGTCGGGGCG GGGGCCGTGG 60
257 CGGAGTCGTC TCGGCGGTGG GTGGCCCGAG AAGGGAGAGA ACGATCGCGG AGCAGGGCGC 120
259 CCGAACTCCG GGGCGCGCGC C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG 171
260 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys
W--> 261      250      255
263 TAC CTG CGC AGC TCG GAA GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC 219
264 Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His
W--> 265      260      265      270
267 GAA GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA 267
268 Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro
W--> 269      275      280      285
271 CCC GCG GCG TCC CGC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG 315
272 Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu
W--> 273      290      295      300
275 GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG 363
276 Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln
W--> 277 305      310      315      320
279 ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA 411
280 Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg
W--> 281      325      330      335

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281 ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG      459
284 Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu
W--> 285          340          345          350
287 AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT      507
288 Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe
W--> 289          355          360          365
291 CAG GGG GGC GTG CAG AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC      555
292 Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg
W--> 293          370          375          380
295 TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC      603
296 Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala
W--> 297 385          390          395          400
299 CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT      651
300 Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn
W--> 301          405          410          415
303 GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG      699
304 Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp
W--> 305          420          425          430
307 TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC      747
308 Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn
W--> 309          435          440          445
311 GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC      795
312 Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn
W--> 313          450          455          460
315 AIT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT      843
316 Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr
W--> 317 465          470          475          480
319 CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT      891
320 Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser
W--> 321          485          490          495
323 ICT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT      939
324 Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn
W--> 325          500          505          510
327 ICT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC      987
328 Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu
W--> 329          515          520          525
331 CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG      1035
332 Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu
W--> 333          530          535          540
335 GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC      1083
336 Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp
W--> 337 545          550          555          560
339 ATA GAC TGA GATCATTTTC GTGGAACATT AGCATGGATG TCCTAGATGT      1132
340 Ile Asp *
343 TTGGAAACTT CTTAAAAAAT GGATGATGTC TATACATGTG TAAGACTACT AAGAGACATG      1192
345 GCCCACGGTG TATGAAACTC ACAGCCCTCT CTCTTGAGCC CTGTACAGGT TGTGTATATG      1252
347 TAAAGTCCAT AGGTGATGTT AGATTCAATG TGATTACACA ACGGTTTTAC AATTTTGTAA      1312
349 TGATTTCCTA GAATTGAACC AGATTGGGAG AGGTATTCCG ATGCTTATGA AAAACITACA      1372
351 CGTGAGCTAT GGAAGGGGGT CACAGTCTCT GGTCTAACCC CTGGACATGT GCCACTGAGA      1432

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VERIFICATION SUMMARY

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Input Set : N:\Crif3\RULE60\09873829.raw

Output Set : N:\CRF3\03122002\I873829.raw

L:31 M:220 C Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C Keyword misspelled or invalid format, [(B) FILING DATE:]
L:261 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:265 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:269 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:273 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:277 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:281 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:285 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:289 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:293 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:297 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:301 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:305 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:309 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:313 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:317 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:321 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:325 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:329 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:333 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:337 M:336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3